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RAW SEQUENCE LISTING             DATE:  03/29/2001
PATENT APPLICATION:  US/09/742,684     TIME:  10:59:33

Input Set : N:\Crf3\RULE60\09742684.txt
Output Set: N:\CRF3\03292001\I742684.raw
```

ENTERED

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      SEQUENCE LISTING
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Mathews, Lawrence S.
 6                     Vale, Wylie W.
 7                     Tsuchida, Kunihiro
 9     (ii) TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
10                              RECEPTOR(S) OF THE ACTIVIN/TGF-BETA SUPERFAMILY
12    (iii) NUMBER OF SEQUENCES: 14
14     (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
16          (B) STREET: 444 South Flower Street, Suite 2000
17          (C) CITY: Los Angeles
18          (D) STATE: CA
19          (E) COUNTRY: USA
20          (F) ZIP: 90071
22      (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Floppy disk
24          (B) COMPUTER: IBM PC compatible
25          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28     (vi) CURRENT APPLICATION DATA:
C--> 29          (A) APPLICATION NUMBER: US/09/742,684
C--> 30          (B) FILING DATE: 19-Dec-2000
31          (C) CLASSIFICATION:
48    (vii) PRIOR APPLICATION DATA:
34          (A) APPLICATION NUMBER: 08/476,123
35          (B) FILING DATE:
37          (A) APPLICATION NUMBER: US 08/300,584
38          (B) FILING DATE: 02-SEP-1994
41          (A) APPLICATION NUMBER: US 07/880,220
42          (B) FILING DATE: 08-MAY-1992
45          (A) APPLICATION NUMBER: US 07/773,229
46          (B) FILING DATE: 09-OCT-1991
49          (A) APPLICATION NUMBER: US 07/698,709
50          (B) FILING DATE: 10-MAY-1991
52   (viii) ATTORNEY/AGENT INFORMATION:
53          (A) NAME: Reiter, Stephen E.
54          (B) REGISTRATION NUMBER: 31,192
55          (C) REFERENCE/DOCKET NUMBER: P41 9927
57     (ix) TELECOMMUNICATION INFORMATION:
58          (A) TELEPHONE: 619-546-4737
59          (B) TELEFAX: 619-546-9392
62 (2) INFORMATION FOR SEQ ID NO: 1:
64      (i) SEQUENCE CHARACTERISTICS:
65          (A) LENGTH: 2563 base pairs
66          (B) TYPE: nucleic acid
67          (C) STRANDEDNESS: single
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RAW SEQUENCE LISTING   DATE: 03/29/2001
PATENT APPLICATION: US/09/742,684   TIME: 10:59:33

Input Set : N:\Crf3\RULE60\09742684.txt
Output Set: N:\CRF3\03292001\I742684.raw

```
68              (D) TOPOLOGY: linear
70        (ii) MOLECULE TYPE: cDNA
73        (ix) FEATURE:
74              (A) NAME/KEY: CDS
75              (B) LOCATION: 71..1609
78        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80 CTCCGAGGAA GACCCAGGGA ACTGGATATC TAGCGAGAAC TTCCTACGGC TTCTCCGGCG       60
82 CCTCGGGAAA ATG GGA GCT GCT GCA AAG TTG GCG TTC GCC GTC TTT CTT       109
83              Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu
84              1               5                   10
86 ATC TCT TGC TCT TCA GGT GCT ATA CTT GGC AGA TCA GAA ACT CAG GAG       157
87 Ile Ser Cys Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu
88     15                  20                  25
90 TGT CTT TTC TTT AAT GCT AAT TGG GAA AGA GAC AGA ACC AAC CAG ACT       205
91 Cys Leu Phe Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr
92 30                  35                  40                  45
94 GGT GTT GAA CCT TGC TAT GGT GAT AAA GAT AAA CGG CGA CAT TGT TTT       253
95 Gly Val Glu Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe
96                     50                  55                  60
98 GCT ACC TGG AAG AAT ATT TCT GGT TCC ATT GAA ATA GTG AAG CAA GGT       301
99 Ala Thr Trp Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly
100             65                  70                  75
102 TGT TGG CTG GAT GAT ATC AAC TGC TAT GAC AGG ACT GAT TGT ATA GAA      349
103 Cys Trp Leu Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Ile Glu
104             80                  85                  90
106 AAA AAA GAC AGC CCT GAA GTG TAC TTT TGT TGC TGT GAG GGC AAT ATG      397
107 Lys Lys Asp Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met
108     95                  100                 105
110 TGT AAT GAA AAG TTC TCT TAT TTT CCG GAG ATG GAA GTC ACA CAG CCC      445
111 Cys Asn Glu Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro
112 110                 115                 120                 125
114 ACT TCA AAT CCT GTT ACA CCG AAG CCA CCC TAT TAC AAC ATT CTG CTG      493
115 Thr Ser Asn Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu
116             130                 135                 140
118 TAT TCC TTG GTA CCA CTA ATG TTA ATT GCA GGA ATT GTC ATT TGT GCA      541
119 Tyr Ser Leu Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala
120             145                 150                 155
122 TTT TGG GTG TAC AGA CAT CAC AAG ATG GCC TAC CCT CCT GTA CTT GTT      589
123 Phe Trp Val Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val
124             160                 165                 170
126 CCT ACT CAA GAC CCA GGA CCA CCC CCA CCT TCC CCA TTA CTA GGG TTG      637
127 Pro Thr Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu
128     175                 180                 185
130 AAG CCA TTG CAG CTG TTA GAA GTG AAA GCA AGG GGA AGA TTT GGT TGT      685
131 Lys Pro Leu Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys
132 190                 195                 200                 205
134 GTC TGG AAA GCC CAG TTG CTC AAT GAA TAT GTG GCT GTC AAA ATA TTT      733
135 Val Trp Lys Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe
136             210                 215                 220
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139 CCA ATA CAG GAC AAA CAG TCC TGG CAG AAT GAA TAT GAA GTC TAT AGT      781
140 Pro Ile Gln Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser
141         225             230             235
143 CTA CCT GGA ATG AAG CAT GAG AAC ATA CTA CAG TTC ATT GGT GCA GAG      829
144 Leu Pro Gly Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu
145         240             245             250
147 AAA AGA GGC ACC AGT GTG GAT GTG GAC CTG TGG CTA ATC ACA GCA TTT      877
148 Lys Arg Gly Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe
149         255             260             265
151 CAT GAA AAG GGC TCA CTG TCA GAC TTT CTT AAG GCT AAT GTG GTC TCT      925
152 His Glu Lys Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser
153 270             275             280             285
155 TGG AAT GAA CTT TGT CAT ATT GCA GAA ACC ATG GCT AGA GGA TTG GCA      973
156 Trp Asn Glu Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala
157             290             295             300
159 TAT TTA CAT GAG GAT ATA CCT GGC TTA AAA GAT GGC CAC AAG CCT GCA     1021
160 Tyr Leu His Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala
161             305             310             315
163 ATC TCT CAC AGG GAC ATC AAA AGT AAA AAT GTG CTG TTG AAA AAC AAT     1069
164 Ile Ser His Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn
165             320             325             330
167 CTG ACA GCT TGC ATT GCT GAC TTT GGG TTG GCC TTA AAG TTC GAG GCT     1117
168 Leu Thr Ala Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala
169         335             340             345
171 GGC AAG TCT GCA GGT GAC ACC CAT GGG CAG GTT GGT ACC CGG AGG TAT     1165
172 Gly Lys Ser Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr
173 350             355             360             365
175 ATG GCT CCA GAG GTG TTG GAG GGT GCT ATA AAC TTC CAA AGG GAC GCA     1213
176 Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala
177             370             375             380
179 TTT CTG AGG ATA GAT ATG TAC GCC ATG GGA TTA GTC CTA TGG GAA TTG     1261
180 Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu
181         385             390             395
183 GCT TCT CGT TGC ACT GCT GCA GAT GGA CCC GTA GAT GAG TAC ATG TTA     1309
184 Ala Ser Arg Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu
185         400             405             410
187 CCA TTT GAG GAA GAA ATT GGC CAG CAT CCA TCT CTT GAA GAT ATG CAG     1357
188 Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln
189     415             420             425
191 GAA GTT GTT GTG CAT AAA AAA AAG AGG CCT GTT TTA AGA GAT TAT TGG     1405
192 Glu Val Val Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp
193 430             435             440             445
195 CAG AAA CAT GCA GGA ATG GCA ATG CTC TGT GAA ACG ATA GAA GAA TGT     1453
196 Gln Lys His Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys
197             450             455             460
199 TGG GAT CAT GAT GCA GAA GCC AGG TTA TCA GCT GGA TGT GTA GGT GAA     1501
200 Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu
201             465             470             475
203 AGA ATT ACT CAG ATG CAA AGA CTA ACA AAT ATC ATT ACT ACA GAG GAC     1549
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204 Arg Ile Thr Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp
205         480             485             490
207 ATT GTA ACA GTG GTC ACA ATG GTG ACA AAT GTT GAC TTT CCT CCC AAA       1597
208 Ile Val Thr Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys
209         495             500             505
211 GAA TCT AGT CTA TGATGGTGGC ACCGTCTGTA CACACTGAGG ACTGGGACTC            1649
212 Glu Ser Ser Leu
213 510
215 TGAACTGGAG CTGCTAAGCT AAGGAAAGTG CTTAGTTGAT TTTCTGTGTG AAATGAGTAG       1709
217 GATGCCTCCA GGACATGTAC GCAAGCAGCC CCTTGTGGAA AGCATGGATC TGGGAGATGG       1769
219 ATCTGGGAAA CTTACTGCAT CGTCTGCAGC ACAGATATGA AGAGGAGTCT AAGGGAAAAG       1829
221 CTGCAAACTG TAAAGAACTT CTGAAAATGT ACTCGAAGAA TGTGGCCCTC TCCAAATCAA       1889
223 GGATCTTTTG GACCTGGCTA ATCAAGTATT TGCAAAACTG ACATCAGATT TCTTAATGTC       1949
225 TGTCAGAAGA CACTAATTCC TTAAATGAAC TACTGCTATT TTTTTTAAAT GAAAAACTTT       2009
227 TCATTTCAGA TTTTAAAAAG GGTAACTTTT TATTGCATTT GCTGTTGTTT CTATAAATGA       2069
229 CTATTGTAAT GCCAACATGA CACAGCTTGT GAATGTGTAG TGTGCTGCTG TTCTGTGTAC       2129
231 ATAGTCATCA AAGTGGGGTA CAGTAAAGAG GCTTCCAAGC ATTACTTTAA CCTCCCTCAA       2189
233 CAAGGTATAC CTCAGTTCCA CGGTTGTTAA ATTATAAAAT TGAAAACACT AACAGAATTT       2249
235 GAATAAATCA GTCCATGTTT TATAACAAGG TTAATTACAA ATTCACTGTG TTATTTAAGA       2309
237 AAAAATGGTA AGCTATGCTT AGTGCCAATA GTAAGTGGCT ATTTGTAAAG CAGTGTTTTA       2369
239 GCTTTTCTTC TACTGGCTTG TAATTTAGGG AAAACAAGTG CTGTCTTTGA AATGGAAAAG       2429
241 AATATGGTGT CACCCTACCC CCCATACTTA TATCAAGGTC CCAAAATATT CTTTTCCATT       2489
243 TCAAAGACAG CACTTTGAAA ACCCTAAATT ACAAGCCAGT AGAAGAAAAG CTAAAACACG       2549
245 CTTTACAAAT AGCC                                                        2563
248 (2) INFORMATION FOR SEQ ID NO: 2:
250     (i) SEQUENCE CHARACTERISTICS:
251         (A) LENGTH: 513 amino acids
252         (B) TYPE: amino acid
253         (D) TOPOLOGY: linear
255     (ii) MOLECULE TYPE: protein
257     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
259 Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
260  1               5               10              15
262 Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
263             20              25              30
265 Phe Asn Ala Asn Trp Glu Arg Asp Arg Thr Asn Gln Thr Gly Val Glu
266         35              40              45
268 Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
269     50              55              60
271 Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
272 65              70              75              80
274 Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Ile Glu Lys Lys Asp
275             85              90              95
277 Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
278         100             105             110
280 Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
281         115             120             125
283 Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
284         130             135             140
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286 Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
287 145             150             155             160
289 Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
290             165             170             175
292 Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
293             180             185             190
295 Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
296         195             200             205
298 Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
299     210             215             220
301 Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
302 225             230             235             240
304 Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
305             245             250             255
307 Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
308             260             265             270
310 Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
311         275             280             285
313 Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
314         290             295             300
316 Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
317 305             310             315             320
319 Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
320             325         .       330             335
322 Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
323             340             345             350
324 Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
325         355             360             365
327 Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
328     370             375             380
330 Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
331 385             390             395             400
333 Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
334             405             410             415
336 Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
337             420             425             430
340 Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His
341         435             440             445
343 Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
344     450             455             460
346 Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
347 465             470             475             480
349 Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
350             485             490             495
352 Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
353             500             505             510
355 Leu
358 (2) INFORMATION FOR SEQ ID NO: 3:
360      (i) SEQUENCE CHARACTERISTICS:
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VERIFICATION SUMMARY   DATE: 03/29/2001
PATENT APPLICATION: **US/09/742,684**   TIME: 10:59:34

Input Set : **N:\Crf3\RULE60\09742684.txt**
Output Set: **N:\CRF3\03292001\I742684.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10